AMENDMENTS TO THE SPECIFICATION

Please amend the paragraph starting at page 6, line 1 as follows:

FIG. 2. Nucleotide and deduced amino acid sequences of human PHELIX cDNA (clone GTP1C12) (SEQ ID NO: 1 and SEQ ID NO: 2, respectively). The sequence surrounding the start ATG (AAC ATG G) exhibits a Kozak sequence (A at position -3, and G at position +1). The putative bHLH domain is underlined in bold, and two putative nuclear localization signals are boxed and shaded.

Please amend the paragraph starting at page 6, line 8 as follows:

FIG. 3. Amino acid sequence alignment of human PHELIX with the bHLH domains of the transcription factors Max and Mxi, (SEQ ID NO: 3 and SEQ ID NO: 4, respectively), showing a 60% similarity to Max over a 50 amino acid region, and a 70% similarity to Mxi over a 24 amino acid region.

Please amend the paragraph starting at page 9, line 29 as follows:

A schematic diagram of the PHELIX protein structure is shown in FIG. 1 and the cDNA sequence of the human PHELIX gene and amino acid sequence of the encoded PHELIX protein are shown in FIG. 2 (SEQ ID NO: 1 and SEQ ID NO: 2, respectively). PHELIX is a 405 amino acid protein containing a bHLH domain and two putative nuclear localization sequences (FIGS. 1 and 2). Recombinant PHELIX is expressed as a 48 kD protein in a mammalian expression system. The human PHELIX gene maps to chromosome 13q13.1-13.3. The PHELIX protein localizes primarily in the nucleus.

Please amend the paragraph starting at page 10, line 18 as follows:

A PHELIX polynucleotide may comprise a polynucleotide having the nucleotide sequence of human PHELIX as shown in FIG. 2, (SEQ ID NO: 2), wherein T can also be U; a polynucleotide which encodes all or part of the PHELIX protein; a sequence complementary to the foregoing; or a polynucleotide fragment of any of the foregoing. Another embodiment comprises a polynucleotide having the sequence as shown in FIG. 2, (SEQ ID NO: 1), from nucleotide residue number 735

through nucleotide residue number 1949, wherein T can also be U. Another embodiment comprises a polynucleotide encoding a PHELIX polypeptide whose sequence is encoded by the cDNA contained in the plasmid as deposited with American Type Culture Collection as Accession No. 98956. Another embodiment comprises a polynucleotide which is capable of hybridizing under stringent hybridization conditions to the human PHELIX cDNA shown in FIG. 2, (SEQ ID NO: 1), or to a polynucleotide fragment thereof.

Please amend the paragraph starting at page11, line 1 as follows:

Further specific embodiments of this aspect of the invention include primers and primer pairs, which allow the specific amplification of the polynucleotides of the invention or of any specific parts thereof, and probes that selectively or specifically hybridize to nucleic acid molecules of the invention or to any part thereof. Probes may be labeled with a detectable marker, such as, for example, a radioisotope, fluorescent compound, bioluminescent compound, a chemiluminescent compound, metal chelator or enzyme. Such probes and primers can be used to detect the presence of a PHELIX polynucleotide in a sample and as a means for detecting a cell expressing a PHELIX protein. Examples of such probes include polypeptides comprising all or part of the human PHELIX cDNA sequence shown in FIG. 2, (SEQ ID NO: 1). Examples of primer pairs capable of specifically amplifying PHELIX mRNAs are also described in the Examples which follow. As will be understood by the skilled artisan, a great many different primers and probes may be prepared based on the sequences provided in herein and used effectively to amplify and/or detect a PHELIX mRNA.

Please amend the paragraph starting at page 11, line 32 as follows:

The PHELIX cDNA sequences described herein enable the isolation of other polynucleotides encoding PHELIX gene product(s), as well as the isolation of polynucleotides encoding PHELIX gene product homologues, alternatively spliced isoforms, allelic variants, and mutant forms of the PHELIX gene product. Various molecular cloning methods that can be employed to isolate full length cDNAs encoding a PHELIX gene are well known (See, for example, Sambrook, J. et al, Molecular Cloning: A Laboratory Manual, 2d edition., Cold Spring Harbor Press, New York, 1989;

Current Protocols in Molecular Biology. Ausubel et al., Eds., Wiley and Sons, 1995). For example, lambda phage cloning methodologies may be conveniently employed, using commercially available cloning systems (e.g., Lambda ZAP Express, Stratagene). Phage clones containing PHELIX gene cDNAs may be identified by probing with a labeled PHELIX cDNA or a fragment thereof. For example, in one embodiment, the PHELIX cDNA (FIG. 2) (SEQ ID NO: 2), or a portion thereof can be synthesized and used as a probe to retrieve overlapping and full length cDNAs corresponding to a PHELIX gene. The PHELIX gene itself may be isolated by screening genomic DNA libraries, bacterial artificial chromosome libraries (BACs), yeast artificial chromosome libraries (YACs), and the like, with PHELIX DNA probes or primers.

Please amend the paragraph starting at page 14, line 13 as follows:

A specific embodiment of a PHELIX protein comprises a polypeptide having the amino acid sequence of human PHELIX as shown in FIG. 2 (SEQ ID NO: 2).

Please amend the paragraph starting at page 15, line 16 as follows:

The invention also provides PHELIX polypeptides comprising biologically active fragments of the PHELIX amino acid sequence, such as a polypeptide corresponding to part of the amino acid sequences for PHELIX as shown in FIG. 2 (SEQ ID NO: 2). Such polypeptides of the invention exhibit properties of the PHELIX protein, such as the ability to elicit the generation of antibodies which specifically bind an epitope associated with the PHELIX protein.

Please amend the paragraph starting at page 17, line 13 as follows:

Various methods for the preparation of antibodies are well known in the art. For example, antibodies may be prepared by immunizing a suitable mammalian host using a PHELIX protein, peptide, or fragment, in isolated or immunoconjugated form (Antibodies: A Laboratory Manual, CSH Press, Eds., Harlow, and Lane (1988); Harlow, Antibodies, Cold Spring Harbor Press, NY (1989)). In addition, fusion proteins of PHELIX may also be used, such as a PHELIX GST-fusion protein. In a particular embodiment, a GST fusion protein comprising all or most of the open reading frame amino acid sequence of FIG. 2, (SEQ ID NO: 2), may be produced and used as an

immunogen to generate appropriate antibodies. In another embodiment, a PHELIX peptide may be synthesized and used as an immunogen. As described in Example 5, below, the 15-mer PHELIX peptide HSSKEKLRRERIKYC was conjugated to keyhole limpet hemocyanin (KLH) and used to immunize a rabbit. The resulting polyclonal antiserum specifically recognized PHELIX expressed in a recombinant mammalian expression system.

Please amend the paragraph starting at page 17, line 32 as follows:

The amino acid sequence of PHELIX as shown in FIG. 2 (SEQ ID NO: 2) may be used to select specific regions of the PHELIX protein for generating antibodies. For example, hydrophobicity and hydrophilicity analyses of the PHELIX amino acid sequence may be used to identify hydrophilic regions in the PHELIX structure. Regions of the PHELIX protein that show immunogenic structure, as well as other regions and domains, can readily be identified using various other methods known in the art, such as Chou-Fasman, Gamier-Robson, Kyte-Doolittle, Eisenberg, Karplus-Schultz or Jameson-Wolf analysis. Methods for the generation of PHELIX antibodies are further illustrated by way of the examples provided herein.

Please amend the paragraph starting at page 20, line 1 as follows:

In one embodiment, a method for detecting a PHELIX mRNA in a biological sample comprises producing cDNA from the sample by reverse transcription using at least one primer; amplifying the cDNA so produced using a PHELIX polynucleotides as sense and antisense primers to amplify PHELIX cDNAs therein; and detecting the presence of the amplified PHELIX cDNA. In another embodiment, a method of detecting a PHELIX gene in a biological sample comprises first isolating genomic DNA from the sample; amplifying the isolated genomic DNA using PHELIX polynucleotides as sense and antisense primers to amplify the PHELIX gene therein; and detecting the presence of the amplified PHELIX gene. Any number of appropriate sense and antisense probe combinations may be designed from the nucleotide sequences provided for PHELIX (FIG. 2, SEQ ID NO: 2,) and used for this purpose.

Please amend the paragraph starting at page 31, line 7 as follows:

DPNCDN (cDNA synthesis primer) (SEQ ID NO: 5):

Please amend the paragraph starting at page 31, line 10 as follows:

Adaptor 1 (SEQ ID NO: 6):

Please amend the paragraph starting at page 31, line 13 as follows:

Adaptor 2 (SEQ ID NO: 7):

Please amend the paragraph starting at page 31, line 16 as follows:

PCR primer 1 (SEQ ID NO: 8):

Please amend the paragraph starting at page 31, line 19 as follows:

Nested primer (NP)1 (SEQ ID NO: 9):

Please amend the paragraph starting at page 31, line 22 as follows:

Nested primer (NP)2 (SEQ ID NO: 10):

Please amend the paragraph starting at page 33, line 18 as follows:

Normalization of the first strand cDNAs were from multiple tissues was performed by using the primers 5'atatcgccgcgctcgtcgtcgacaa3' (SEQ ID NO: 13) and 5'agccacacgcagctcattgtagaagg 3' (SEQ ID NO: 14) to amplify β-actin. First strand cDNA (5 μl) was amplified in a total volume of 50 μl containing 0.4 μM primers, 0.2 μM each dNTPs, 1XPCR buffer (Clontech, 10 mM Tris-HCL, 1.5 mM $MgCl_2$, 50 mM KCI, pH8.3) and 1X Klentaq DNA polymerase (Clontech). Five μl of the PCR reaction was removed at 18, 20, and 22 cycles and used for agarose gel electrophoresis. PCR was performed using an MJ Research thermal cycler under the following conditions: initial denaturation was at 94°C for 15 sec, followed by a 18, 20, and 22 cycles of 94°C for 15, 65°C for 2 min, 72°C for 5 sec. A final extension at 72°C was carried out for 2 min. After agarose gel electrophoresis, the band intensities of the 283 bp β-actin bands from multiple tissues were

compared by visual inspection. Dilution factors for the first strand cDNAs were calculated to result in equal β-actin band intensities in all tissues after 22 cycles of PCR. Three rounds of normalization were required to achieve equal band intensities in all tissues after 22 cycles of PCR.

Please amend the paragraph starting at page 34, lines 1-2 as follows:

5'- CTG CGT ACT CTC TTG CCG TAT GT -3' (SEQ ID NO: 11)

5'- GCT CAA TGG GTG TTT GTT GTT TCT-3'(SEQ ID NO: 12)

Please amend the paragraph starting at page 38, lines 10-11 as follows:

22P4G9.1 5'- CTG CGT ACT CTC TTG CCG TAT GT -3' (SEQ ID NO: 11)

22P4G9.2 5'- GCT CAA TGG GTG TTT GTT GTT TCT-3'(SEQ ID NO: 12)